

WEST**Help Logout Interrupt****Main Menu Search Form Posting Counts Show S Numbers Edit S Numbers Preferences****Search Results -**

Terms	Documents
13 same (conjugat\$ or fuse\$)	10

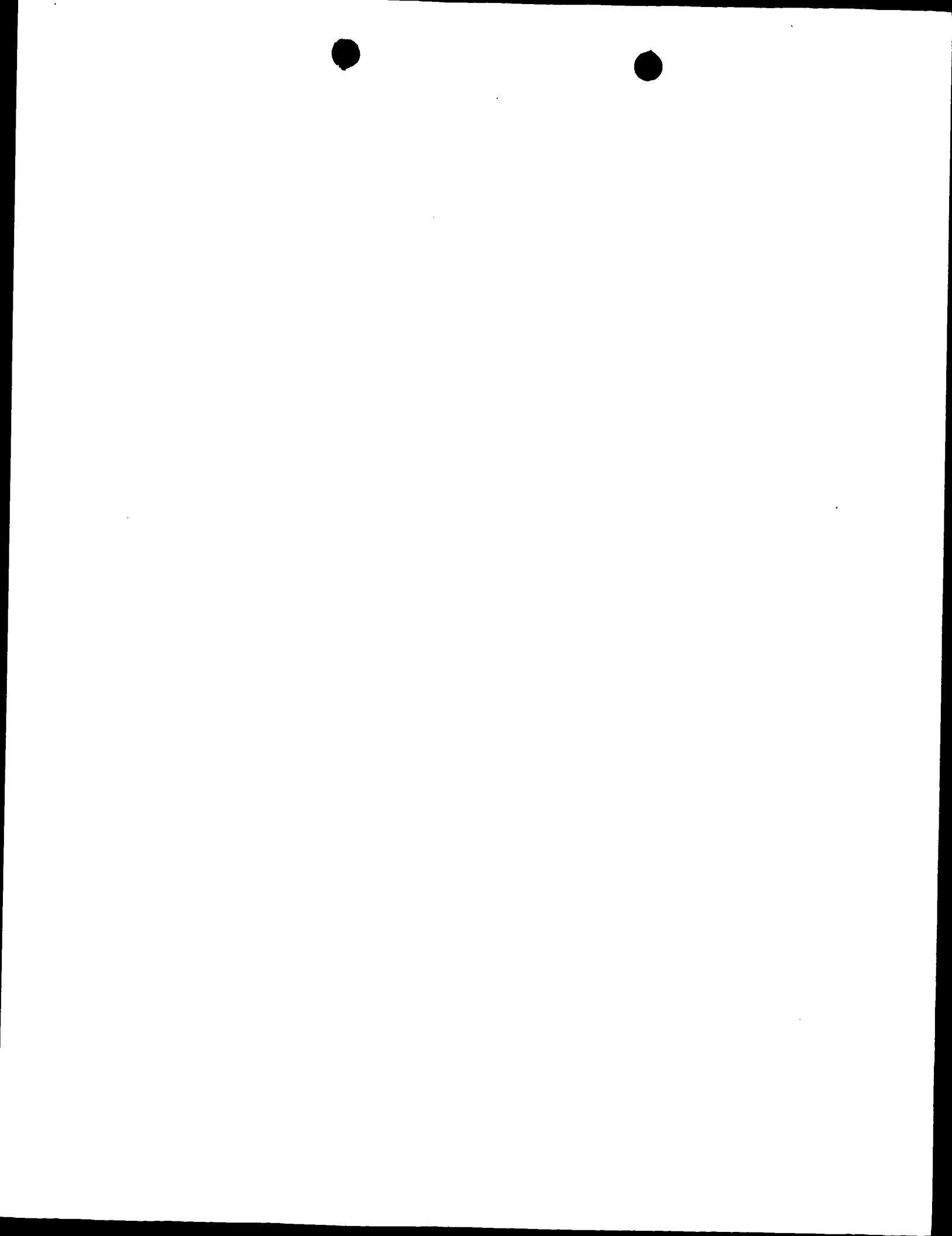
Database:

13 same (conjugat\$ or fuse\$)

Search History**Today's Date: 1/17/2002**

<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
USPT	13 same (conjugat\$ or fuse\$)	10	L4
USPT	12 same peptide\$	66	L3
USPT	albumin\$ same composition\$ same (stability or stable)	548	L2
USPT	fusion adj (protein\$ or polypeptide\$ or polyprotein\$)	12092	L1

09/424,080



(FILE 'HOME' ENTERED AT 12:50:47 ON 17 JAN 2002)

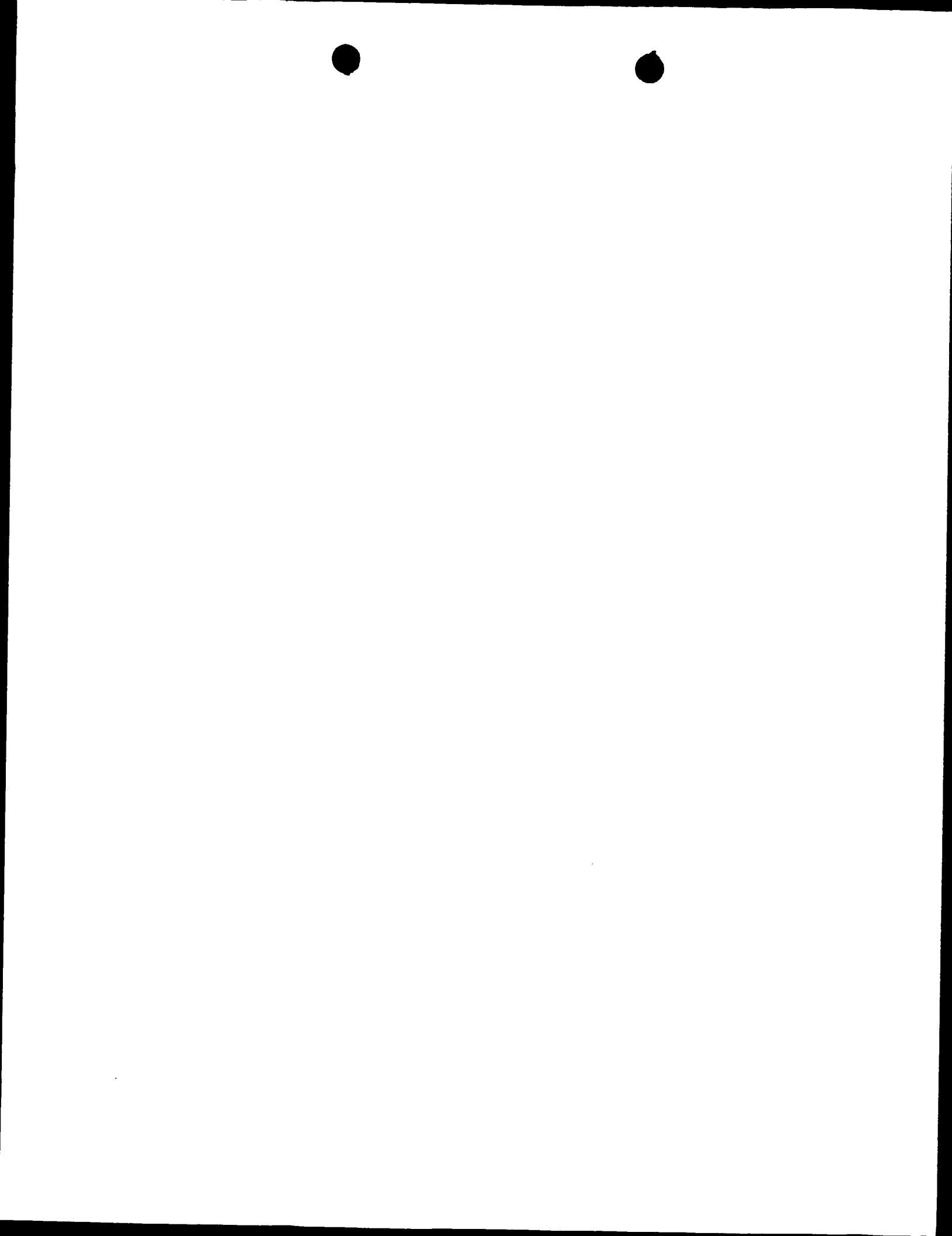
FILE 'MEDLINE' ENTERED AT 12:50:55 ON 17 JAN 2002

L1 128 S ALBUMIN (P) (STABILITY OR STABLE) (P) PEPTIDE?
L2 20 S L1 AND (FUSION? OR CONJUGATE?)
L3 20 DUP REM L2 (0 DUPLICATES REMOVED)

=>

09|424,080

1/17/02.



=> d his

(FILE 'HOME' ENTERED AT 13:45:18 ON 17 JAN 2002)
SET COST OFF

FILE 'REGISTRY' ENTERED AT 13:45:27 ON 17 JAN 2002
L1 138 S LTEKKYSP/SQSP
L2 1 S L1 AND 8/SQL

FILE 'HCAOLD' ENTERED AT 13:45:45 ON 17 JAN 2002
L3 0 S L2

FILE 'HCAPLUS' ENTERED AT 13:45:48 ON 17 JAN 2002
L4 1 S L2

FILE 'USPATFULL, USPAT2' ENTERED AT 13:46:04 ON 17 JAN 2002
L5 0 S L2

=> fil reg
FILE 'REGISTRY' ENTERED AT 13:46:19 ON 17 JAN 2002
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STRUCTURE FILE UPDATES: 15 JAN 2002 HIGHEST RN 383362-48-9
DICTIONARY FILE UPDATES: 15 JAN 2002 HIGHEST RN 383362-48-9

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES
for more information. See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d 12 sqide can

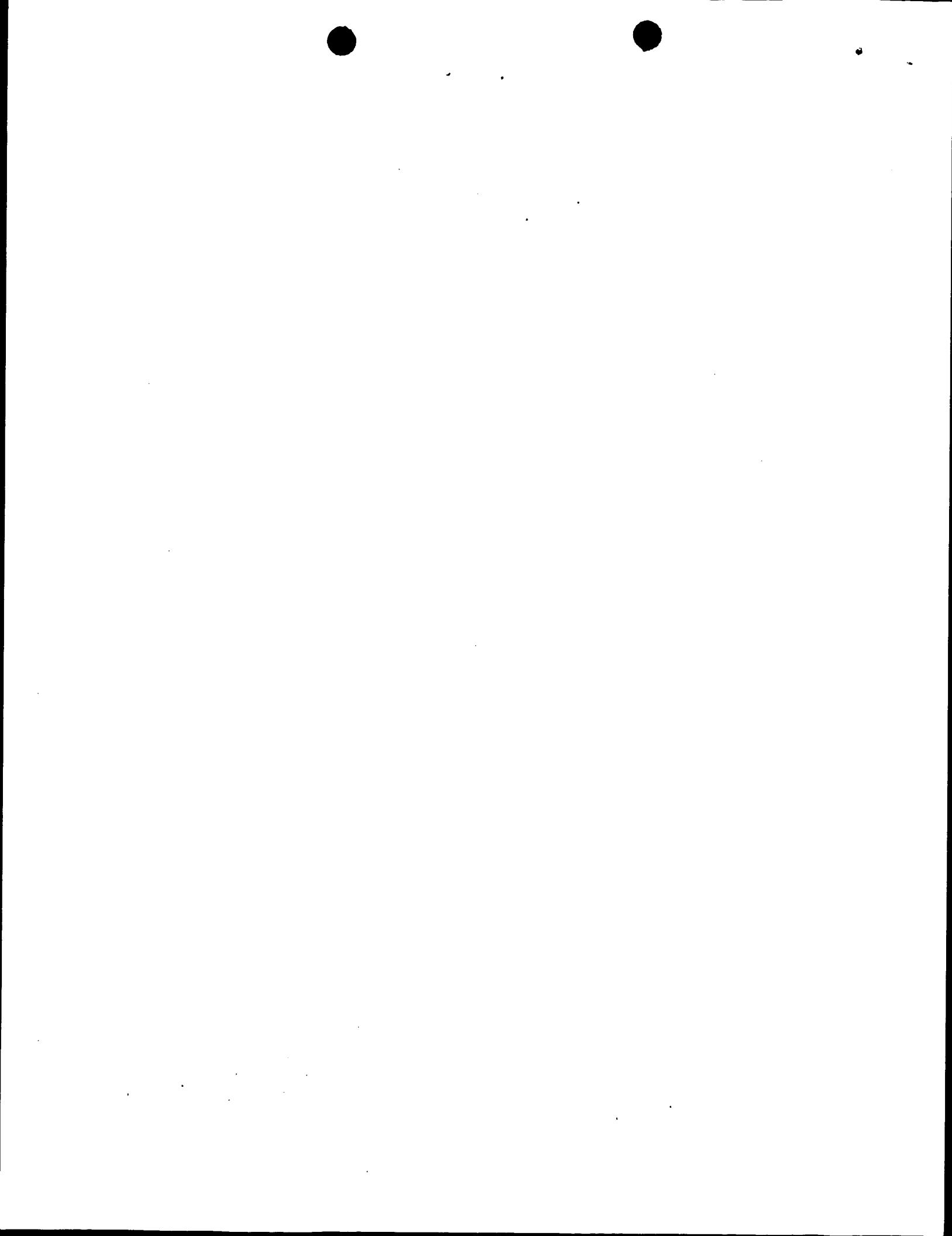
L2 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS
RN 216579-39-4 REGISTRY
CN L-Proline, L-leucyl-L-threonyl-L-.alpha.-glutamyl-L-lysyl-L-lysyl-L-
tyrosyl-L-seryl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 8

SEQ 1 LTEKKYSP
=====

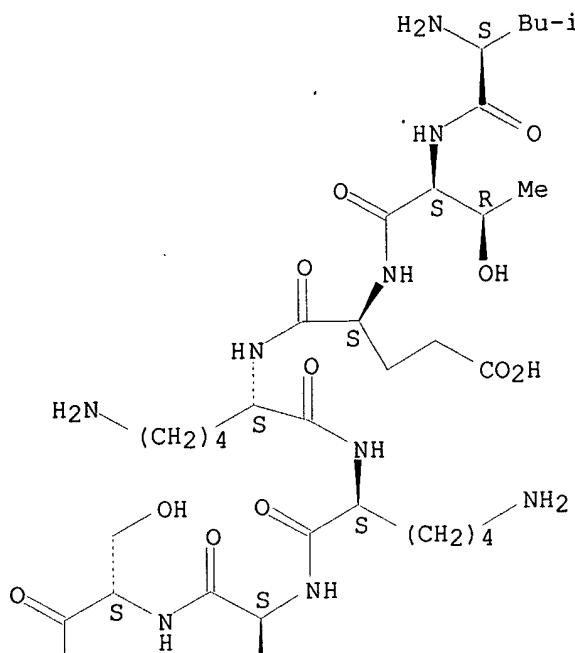
HITS AT: 1-8
MF C44 H72 N10 O14
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, TOXLIT

Absolute stereochemistry.

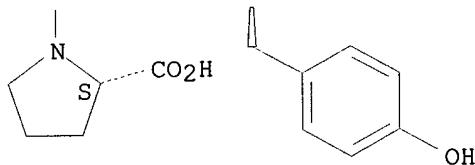
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PAGE 1-A



PAGE 2-A



1 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:33014

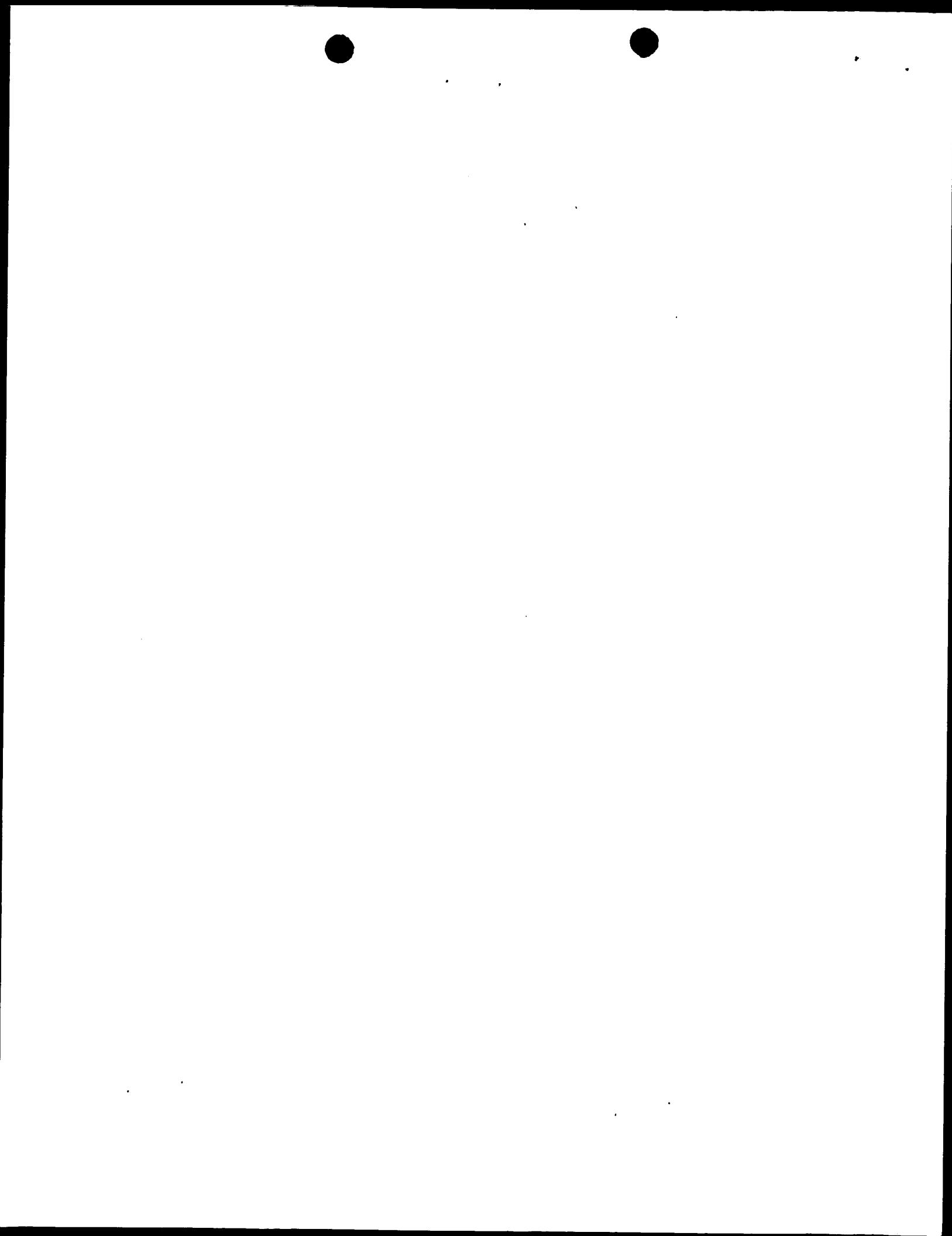
=> fil hcaplus
 FILE 'HCAPLUS' ENTERED AT 13:46:26 ON 17 JAN 2002
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FILE COVERS 1907 - 17 Jan 2002 VOL 136 ISS 3
 FILE LAST UPDATED: 16 Jan 2002 (20020116/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of



all substance data from the REGISTRY file. Enter HELP FIRST for more information.

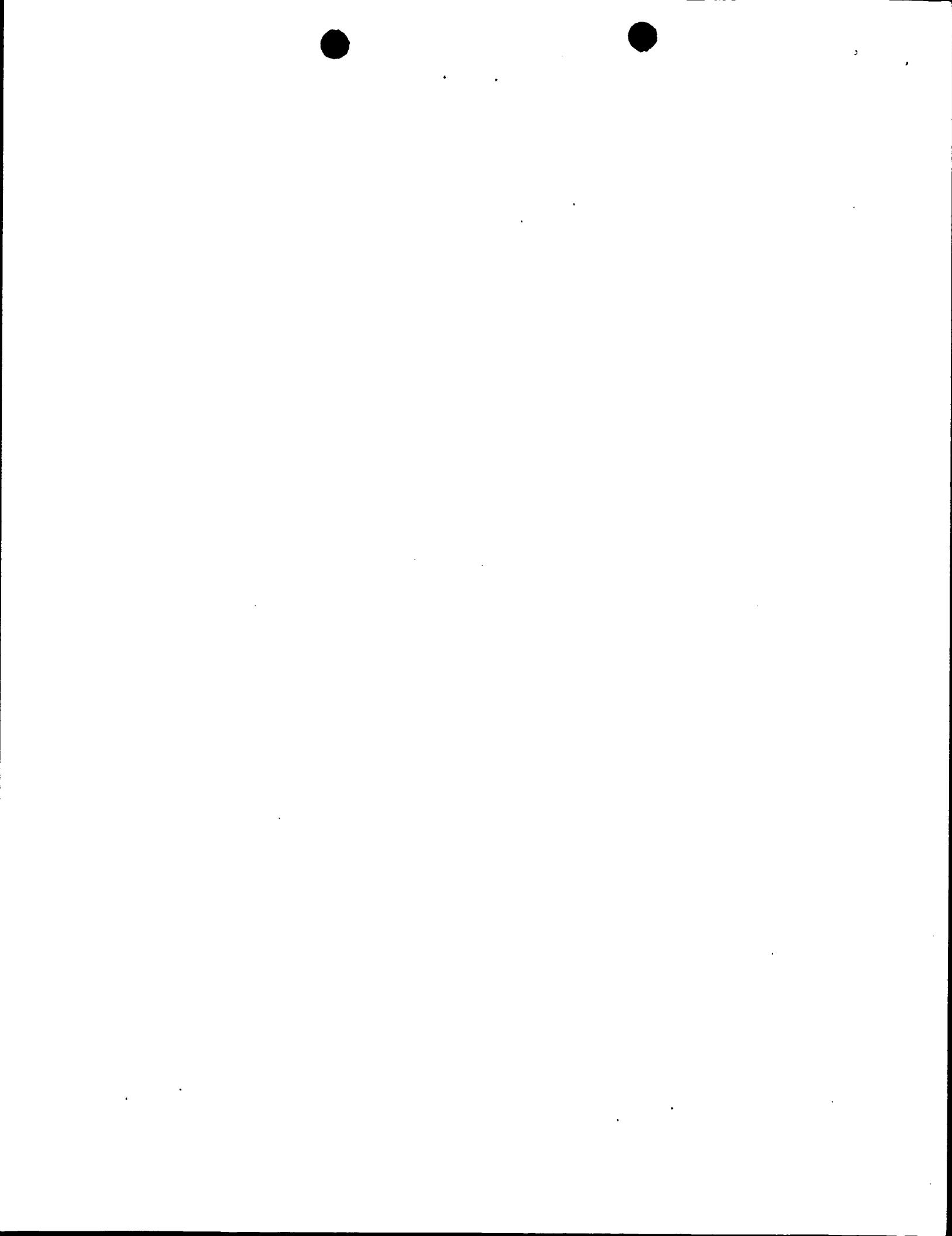
HCAplus now provides online access to patents and literature covered in CA from 1907 to the present. Bibliographic information and abstracts were added in 2001 for over 3.8 million records from 1907-1966.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

=> d 14 all

L4 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
 AN 1998:789037 HCAPLUS
 DN 130:33014
 TI Compositions for enhancing immunosuppressants pharmaceutical activities
 IN Zavialov, Vladimir Petrovich; Vasilenko, Raisa Nikolaevna; Dolgikh, Dmitry Aleksandrovich; Kirpichnikov, Mikhail Petrovich; Navolotskaya, Elena Vitalievna; Korpela, Timo Kalevi
 PA Russia
 SO PCT Int. Appl., 26 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 IC ICM A61K038-04
 ICS A61K038-13; A61K038-21
 CC 1-7 (Pharmacology)
 Section cross-reference(s): 15

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9852594	A1	19981126	WO 1998-FI418	19980518
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	FI 9702121	A	19981120	FI 1997-2121	19970519
	AU 9874352	A1	19981211	AU 1998-74352	19980518
	EP 981359	A1	20000301	EP 1998-921528	19980518
	R: AT, DE, ES, FR, GB, IT, SE, FI				
	JP 2001526675	T2	20011218	JP 1998-550009	19980518
PRAI	FI 1997-2121	A	19970519		
	WO 1998-FI418	W	19980518		
AB	The present invention provides compns. for efficient amplification of immunosuppressive activity of cyclosporins, FK506 or rapamycin to decrease therapeutical dose of immunosuppressants and, as a consequence, avoidance of their undesirable side effects during organ and tissue transplantation, and treatment of different diseases. These compns. include cyclosporins, FK506 or rapamycin and biol. active peptides corresponding to the high-affinity binding/anti-lymphoproliferative site of IFNs-a,b,w,t, or recombinant proteins having the amino acid sequences corresponding to the said site.				
ST	immunosuppressant adjuvant formulation peptide				
IT	Interferon .tau. Interferon .alpha. Interferon .beta.				
RL:	PRP (Properties) (antilymphoproliferative site of; compns. for enhancing				



immunosuppressant pharmaceutical activities)

IT Adenocarcinoma inhibitors
Anti-inflammatory drugs
Antirheumatic drugs
Autoimmune diseases
Drug bioavailability
Immunosuppressants
Leukemia inhibitors
Lupus erythematosus
Lymphoma inhibitors
Myasthenia gravis
Psoriasis
Transplant (organ)
Uveitis
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT Interferon .alpha.2
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT Peptides, biological studies
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(compns. for enhancing immunosuppressant pharmaceutical activities)

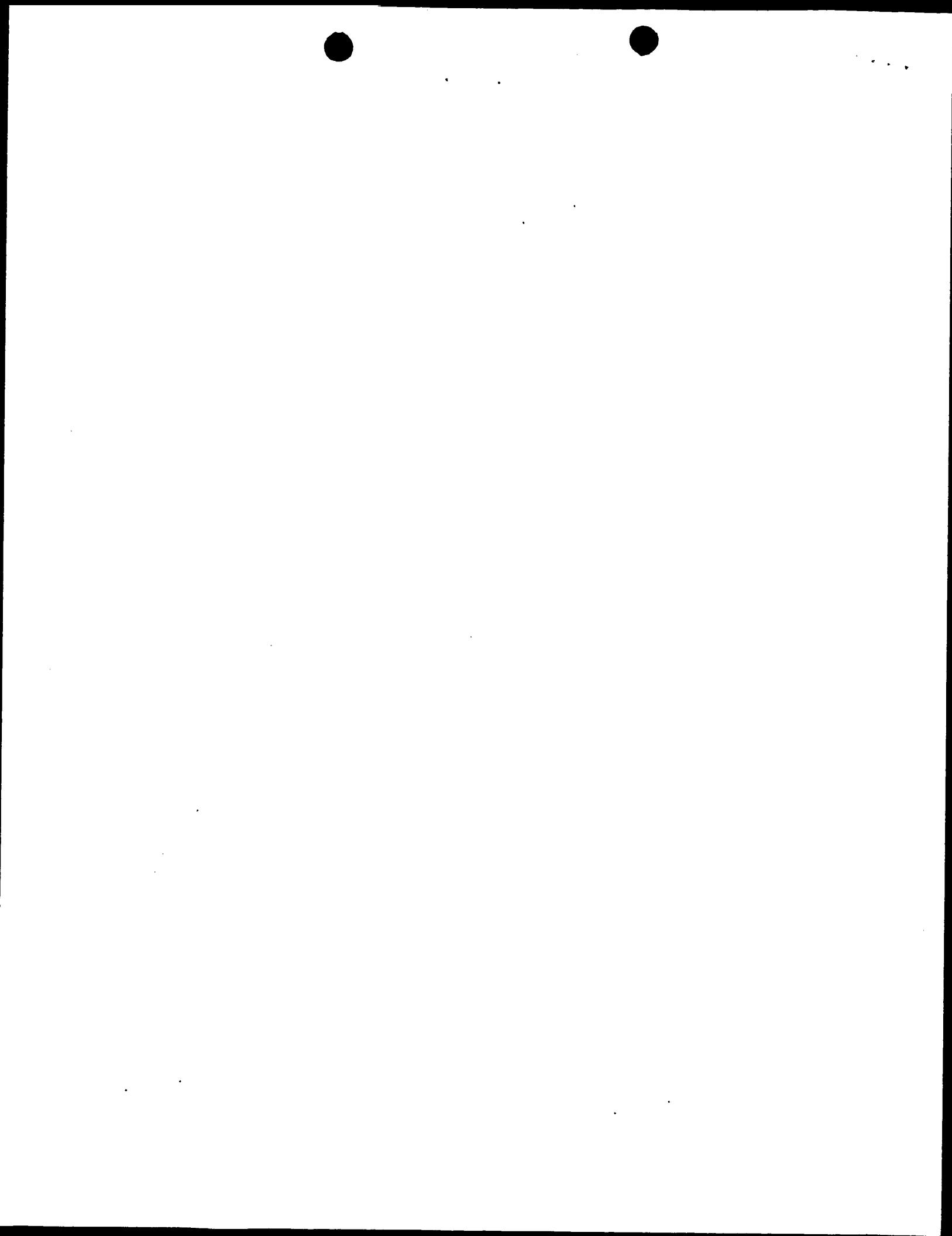
IT Interferons
RL: PRP (Properties)
(interferon .omega., antilymphoproliferative site of; compns. for enhancing immunosuppressant pharmaceutical activities)

IT Antitumor agents
(myeloma; compns. for enhancing immunosuppressant pharmaceutical activities)

IT 216579-39-4D, analogs 216579-44-1D, analogs
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT 53123-88-9, Rapamycin 79217-60-0D, Cyclosporin, derivs. 104987-11-3, Fk506
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(compns. for enhancing immunosuppressant pharmaceutical activities)

RE.CNT 5
RE
(1) University of Florida; WO 9009806 A2 1990 HCPLUS
(2) University of Florida; WO 9410313 A2 1994 HCPLUS
(3) Vacsyn, S; FR 2706772 A1 1994 HCPLUS
(4) Zarogoulidis, K; Lung Cancer 1996, V15(2), P197 MEDLINE
(5) Zav'Yalov, V; Mol Immunol 1995, V32(6), P425 HCPLUS



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:35 ; Search time 12.72 Seconds
(without alignments)
47.909 Million cell updates/sec

Title: US-09-424-080A-1
perfect score: 42
Sequence: 1 LTEKKVSP 8

Scoring table: - BLOSUM62

Gapov 10.0 , Gapext 0.5

Searched: 219241 seqs, 7617552 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-68;*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	21	50.0	8	S21663	neuropeptide - flower beetle (Pachnoda marginata)
2	18	42.9	6	S11556	C;Species: Pachnoda marginata C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
3	18	42.9	8	S15422	C;Accession: S21663 R;Graede, G.; Lopata, A.; Keillner, R.; Rinehart, K.L.
4	18	42.9	8	A50641	A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of va electrometry. A;Reference number: S21663; MUID:92265187
5	17	40.5	8	A03169	A;Accession: S21663 A;Status: preliminary A;Molecule type: protein A;Residues: 1-8 <GAE>
6	16	38.1	5	G7196	Query Match Similarity 50.0%; Score 21; DB 2; Length 8; Best Local Similarity 66.7%; Pred. No. 2.2e+05; Mismatches 0; Indels 0; Gaps 0;
7	16	38.1	6	B4510	Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
8	16	38.1	8	S20162	RESULT 2
9	16	38.1	8	A14683	S11556 hydrogen sulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment) N;Alternate names: bisulfite reductase; desulfotofuscidin C;Species: Desulfovibrio thermophilus C;Date: 19-Mar-1997 #sequence_revision 12-dec-1997 #text_change 30-Jan-1998
10	16	38.1	8	S45651	C;Accession: S11556 R;Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G. Biolchim. Biophys. Acta 1040, 112-118, 1990 A;Title: Purification and characterization of bisulfite reductase (desulfotofuscidin) f A;Reference number: S11024; MUID:9035276
11	14	33.3	5	I1H0A	A;Accession: S11556 A;Molecule type: protein A;Residues: 1-16 <FAI> A;Keywords: oxidoreductase
12	14	33.3	5	A64111	Query Match Similarity 42.9%; Score 18; DB 2; Length 6; Best Local Similarity 75.0%; Pred. No. 2.2e+05; Mismatches 0; Indels 0; Gaps 0;
13	14	33.3	7	P70087	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
14	14	33.3	7	S19027	Db 2 PEKY 5
15	14	33.3	7	PD0029	Db 2 PEKY 5
16	14	33.3	8	A61348	Db 2 PEKY 5
17	14	33.3	8	S0895	Db 2 PEKY 5
18	14	33.3	8	A43823	Db 2 PEKY 5
19	14	33.3	8	A44960	Db 2 PEKY 5
20	14	33.3	8	A43976	Db 2 PEKY 5
21	14	33.3	8	S11545	Db 2 PEKY 5
22	14	33.3	8	S11545	Db 2 PEKY 5
23	14	33.3	8	D47393	Db 2 PEKY 5
24	14	33.3	8	PN0150	Db 2 PEKY 5
25	12	28.6	5	PQ0589	Db 2 PEKY 5
26	12	28.6	7	S17976	Db 2 PEKY 5
27	12	28.6	8	S16324	Db 2 PEKY 5
28	12	28.6	8	A2967	Db 2 PEKY 5
29	12	28.6	4	E44823	Db 2 PEKY 5
11					Db 2 PEKY 5

copper resistance
major protein anti-T-cell receptor
amelelin - rat
mosquitocidal toxin
contraction-inhibitor
T-cell receptor beta
laminin BI - westie
fatty acid synthias
Ig kappa chain V-I
agrecan - bovine
DNA topoisomerase
T-cell receptor beta
virotoxin - destro
hypertrehalosemic

RESULT 3
S15422 adipokinetic hormone - cockchafer
C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997
C;Accession: S15422
R;Gede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-peptide
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (NRP) #status experimental

Query Match 42.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YSP 8
Db 4 YSP 6

RESULT 4
A5841 adipokinetic hormone - dor beetle
C;Species: Goetrupes stercorosus (dor beetle)
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: A5841
R;Gede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-peptide
A;Reference number: S15422; MUID:91248100
A;Accession: A5841
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (NRP) #status experimental

Query Match 42.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YSP 8
Db 4 YSP 6

RESULT 5
A05169 neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Accession: A05169
R;Witten, J.L.; Schaffner, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.I.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry
A;Reference number: A90118; MUID:85046530
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Keywords: neuropeptide
A;Accession: S20162
A;Molecule type: DNA

Query Match 38.1%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 EKKY 6
Db 2 EKDY 5

RESULT 6
G37196 bradykinin-potentiating Peptide 7 - island jaracaa
C;Species: Bothrops insularis (island jaracaa)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: G37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptide
A;Reference number: A37196; MUID:90351557
A;Accession: G37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CDN>
C;Keywords: pyroglutamic acid
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 38.1%; Score 16; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 KKYS 8
Db 1 QKWP 5

RESULT 7
B44510 hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)
C;Species: Lactococcus lactis
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C;Accession: B44510
R;Renault, P.; Gaillardin, C.; Heslot, H.
J. Bacteriol. 171, 3108-3114, 1989
A;Title: Product of the Lactococcus lactis gene required for malolactic fermentation
A;Reference number: A44510; MUID:89255069
A;Accession: B44510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6 <BRN>
A;Cross-references: EMBL:M90762

Query Match 38.1%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

us-09-424-080a-1.closed.Esp

RL Biochem. J. 275:671-677(1991).
 RN [2]
 RP
 RC
 SPECIES=C marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=02265187; PubMed=1580453;
 RA Gaede G., Lopata A., Kellner R., Rinkeart K.L. Jr.;
 RT "Primary structures of neuropeptides isolated from the corpora
 cardiacia of various cetonid beetle species determined by
 pulsed-liquid phase sequencing and tandem fast atom bombardment mass
 spectrometry";
 RL Biol. Chem. Hoppe-Seyler 373:1133-1142(1992).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR: S15422; S151522.
 PIR: S21663; S21663.
 DR Interpro: IPR002047; AKH.
 PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 8 AA; 1022 MW; 867AB775RB544736 CRC64;

Query Match
 Best Local Similarity 42.9%; Score 18; DB 1; Length 8;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 YSP 8
 DB 4 YSP 6

RESULT 3
 BPP7_BOTIN STANDARD: PRT; 5 AA.
 ID BPP7_BOTIN
 AC P30425;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, last sequence update)
 DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
 ENZYME INHIBITOR).
 OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 NCBI_TaxID=8723;
 RN [1]
 SEQUENCE
 TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF THE
 BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR: G37196; G37196.
 KW Hypotensive agent; venom.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match
 Best Local Similarity 38.1%; Score 16; DB 1; Length 5;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KKYSP 8
 :|:|:

Db 1 OKWAP 5
 RESULT 4
 ID PRCT_PERAM
 AC PRCT_PERAM
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1985 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE PROCTOLIN.
 OS Periplaneta americana (American cockroach),
 OS Limulus polyphemus (Atlantic horseshoe crab), and
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Articulata; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattoidea; Blattidae; Periplaneta.
 RX NOBL_TaxID=6978, 6850, 6759;
 RN [1]
 RP
 SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=6074708; PubMed=576;
 RA Starrett A.N., Brown B.B.;
 RT in insects.";
 RL Life Sci. 17:1253-1256(1975).
 [2]
 RP
 RC BILOGICAL SOURCE.
 SPECIES=P.americana;
 RX MEDLINE=8122865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron."
 RL Science 213:567-569(1981).
 RN [3]
 RP
 SEQUENCE.
 RC SPECIES=L.polyphemus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groome J.R., Tillingsast E.K., Towley M.A., Vetrov A.'
 RA Watson W.H. II, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shababowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 horseshoe crab Limulus polyphemus";
 RL peptides 11:205-211(1990).
 RN [4]
 RP
 SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=86332789; PubMed=2872661;
 RA Stangier J., Dirksen H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 pericardial organs of the shore crab, Carcinus maenas.";
 RL Peptides 7:67-72(1986).
 CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 DR PIR: A01644; HORHOA.
 DR PIR: A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match
 Best Local Similarity 33.3%; Score 14; DB 1; Length 5;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 5 KYSP 8
 :|:|:
 DB 1 RYLP 4

RESULT 5
 ID ASP2_LACSN
 STANDARD: PRT; 6 AA.

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:50 ; Search time 22.03 Seconds
(without alignments)

53.118 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREML_17; *

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	25	59.5	8 2	Q9R9E0
2	14	33.3	7 13	P82101
3	14	33.3	8 8	Q9TMN4
4	14	33.3	8 8	Q9T2V2
5	14	33.3	8 8	Q9TY1
6	14	33.3	8 10	Q9XGL9
7	14	33.3	8 10	Q9GLB8
8	8	33.3	8 10	Q9STD5
9	13	31.0	8 2	Q9RT2
10	13	31.0	8 12	Q84271
11	12	28.6	8 6	Q9XSY1
12	12	28.6	8 8	Q35792
13	12	28.6	8 11	Q62933
14	11	26.2	7 7	Q54248
15	11	26.2	8 2	Q56429
16	11	26.2	8 2	Q9R5L7
17	11	26.2	8 8	Q5895
18	11	26.2	8 5	P82689
19	11	26.2	8 8	P82929

SEQUENCE FROM N.A.

RP STRAIN=168;

RX MEDLINE=93003529; PUBMED=1391053;

RA Henriques A.O.; de Lencastre H.; Piggett P.J.;

RA Bacillus subtilis morphogene cluster that includes spore is homologous to the mra region of Escherichia coli.;

RT Bioclinie 74-735-748(1992);

DR EMBL; X64258; CAA45556.1; .

OS Bacterium; Fimicutes; Bacillus/Clostridium group;

OC Bacillus/staphylococcus group; Bacillus;

OC NCBI-TaxID=1423;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN=168;

RX MEDLINE=93003529; PUBMED=1391053;

RA Bacillus subtilis morphogene cluster that includes spore is homologous to the mra region of Escherichia coli.;

RT Bioclinie 74-735-748(1992);

DR EMBL; X64258; CAA45556.1; .

FT NON_TER 8 AA: 893 MW: 88

FT SEQUENCE 8 AA: 893 MW: EET5A1A33321B1A6 CRC64;

Query Match 59.5%; Score 25; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.7e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTEKKYSP 8
Db 1 MTTKKYSP 8

RESULT 2

P82101 ID PRELIMINARY; PRT; 7 AA.

P82101 ID P82101; PRT; 7 AA.

P82101 ID P82101; PRT; 7 AA.

01-MAY-2000 (TREMBl. 13, Created)
DT 01-MAY-2000 (TREMBl. 13, Last sequence update)
DT 01-MAY-2000 (TREMBl. 13, Last annotation update)

Q95213 orcytolaagus
Q95213 begonia for
P82541 spinacia ol
P82421 psathyrosta
P93285 hordeum mar
P92210 agropyron c
P92214 amblyopyrum
P92211 australopyr
P92221 bromus iner
P92226 crithmum
P92372 haynaldia v
P92381 hordeum bra
P92387 henrardia p
P92390 heteranthel
P92393 hordeum vul
P92425 pseudoroegn
P92427 peridictyon
P92430 aegilops ta
P92442 taeniatheru
P92440 thinopyrum
P92403 lophopyrum
O44463 agrobacteri
Q9z1e9 neisseria m
Q9r5r0 shigella dy

DE ELECTRIN 5
 OS *litoria rubella* (Desert tree frog);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Buronoidea; Hylidae;
 OC *Litoria*;
 OC NCBI_TAXID=104895;
 RN [1]
 SEQUENCE.
 RP TISSUE="SKIN SECRETION";
 RA Wabnitz, P.A.; Bowie, J.H.; Tyler, M.J.; Wallace, J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from *Litoria
 rubella*.";
 RL Aust. J. Chem. 52:0-0(1999).
 KW Amphibian skin; Amidation.
 FT MOD_RES 7 7 AMIDATION
 SEQUENCE 7 AA; 834 MW; 6DD05076B0B5030 CRC64;

Qy	6 YSP 8	Db	2 YEP 4
RESULT 3			
ID Q9TWN4	PRELIMINARY;	PRT;	8 AA.
AC Q9TWN4;			
DT 01-MAY-2000 (TREMBLrel. 13; Created)			
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)			
DT 01-MAY-2000 (TREMBLrel. 13; Last annotation update)			
DE RBCL PROTEIN (FRAGMENT).			
GN RBCL.			
OS Begonia formosana.			
OG Chloroplast.			
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;			
OC eurosids I; Cucurbitales; Begoniaceae; Begonia.			
NCBI_TAXID=80370;			
[1]			
SEQUENCE FROM N.A.			
RP Chiang, T.Y.;			
RT "Sequence announcement: rbcl_promotor gene in <i>Begonia formosana</i> .";			
RU Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.			
EMBL; AJ009597; CAB2119_1; -.			
KW Chloroplast.			
FT NON_TER 8 8			
SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;			

Query Match 33.3%; Score 14; DB 13; Length 7;
 Best Local Similarity 66.7%; Pred. No. 4.7e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 2; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 2 TEKK 5
 Db 5 TETK 8

Qy	2 TEKK 5	Db	5 TETK 8
RESULT 5			
ID Q9T2Y1	PRELIMINARY;	PRT;	8 AA.
AC Q9T2Y1;			
DT 01-MAY-2000 (TREMBLrel. 13; Created)			
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)			
DT 01-MAY-2000 (TREMBLrel. 13; Last annotation update)			
DE RBCL PROTEIN (FRAGMENT).			
GN RBCL.			
OS Begonia aptera.			
OG Chloroplast.			
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;			
OC eurosids I; Cucurbitales; Begoniaceae; Begonia.			
NCBI_TAXID=71278;			
[1]			
SEQUENCE FROM N.A.			
RP Chiang, T.Y.;			
RT "Sequence announcement: rbcl_promotor gene in <i>Begonia formosana</i> .";			
RU Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.			
EMBL; AJ009603; CAB52086_1; -.			
DR EMBL; AJ009604; CAB52082_1; -.			
DR EMBL; AJ009605; CAB52084_1; -.			
KW Chloroplast.			
FT NON_TER 8 8			
SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;			

Query Match 33.3%; Score 14; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 4.7e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

Qy 2 TEKK 5
 Db 5 TETK 8

Qy	2 TEKK 5	Db	5 TETK 8
RESULT 6			
ID Q9XGL9	PRELIMINARY;	PRT;	8 AA.
AC Q9XGL9;			
DT 01-NOV-1999 (TREMBLrel. 12; Created)			
DT 01-NOV-1999 (TREMBLrel. 12; Last sequence update)			
DE RBCL PROTEIN (FRAGMENT).			
GN RBCL.			
OS Begonia taipeiensis.			

Query Match 33.3%; Score 14; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 4.7e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; MisMatches 1; Indels 0; Gaps 0;

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 17, 2002, 12:12:40 ; Search time 23.54 Seconds
(without alignments)

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Title: US-09-424-080a-1

Perfect score: 42

Sequence: 1 LPEKKYSP 8

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Total number of hits satisfying chosen parameters: 62388
Listing first 45 summaries

Database : A_Geneseq_1101:*

1: /SIDS8/gcadata/geneseq/geneseq/AAI1980.DAT:*

2: /SIDS8/gcadata/geneseq/geneseq/AAI1981.DAT:*

3: /SIDS8/gcadata/geneseq/geneseq/AAI1990.DAT:*

4: /SIDS8/gcadata/geneseq/geneseq/AAI1993.DAT:*

5: /SIDS8/gcadata/geneseq/geneseq/AAI1994.DAT:*

6: /SIDS8/gcadata/geneseq/geneseq/AAI1995.DAT:*

7: /SIDS8/gcadata/geneseq/geneseq/AAI1996.DAT:*

8: /SIDS8/gcadata/geneseq/geneseq/AAI1997.DAT:*

9: /SIDS8/gcadata/geneseq/geneseq/AAI1998.DAT:*

10: /SIDS8/gcadata/geneseq/geneseq/AAI1999.DAT:*

11: /SIDS8/gcadata/geneseq/geneseq/AAI1990.DAT:*

12: /SIDS8/gcadata/geneseq/geneseq/AAI1992.DAT:*

13: /SIDS8/gcadata/geneseq/geneseq/AAI1993.DAT:*

14: /SIDS8/gcadata/geneseq/geneseq/AAI1994.DAT:*

15: /SIDS8/gcadata/geneseq/geneseq/AAI1995.DAT:*

16: /SIDS8/gcadata/geneseq/geneseq/AAI1996.DAT:*

17: /SIDS8/gcadata/geneseq/geneseq/AAI1997.DAT:*

18: /SIDS8/gcadata/geneseq/geneseq/AAI1998.DAT:*

19: /SIDS8/gcadata/geneseq/geneseq/AAI1999.DAT:*

20: /SIDS8/gcadata/geneseq/geneseq/AAI2000.DAT:*

21: /SIDS8/gcadata/geneseq/geneseq/AAI2001.DAT:*

22: /SIDS8/gcadata/geneseq/geneseq/AAI2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT ID	AR59595	AR59595 standard; peptide; 6 AA.
1	26	61.9	6 15	AAR5959	XX	XX	AC AR59595;
2	24	57.1	6 21	AAB36378	XX	XX	DT 14-FEB-1995 (first entry)
3	24	57.1	6 22	AAE0552	XX	XX	DE Peptide signal sequence for treating leukocyte interferon diseases.
4	24	57.1	7 20	AAR9336	XX	XX	KW therapeutic; metabolic interactions; PSS; analogues.
5	24	57.1	7 22	AAB61834	XX	XX	OS Synthetic.
6	57.1	8 16	AAW21215	XX	XX	XX	PN W9416328-A.
7	57.1	8 16	AAW21216	XX	XX	XX	PD 21-JUL-1994.
8	50.0	8 14	AAR36175	XX	XX	XX	PF 30-DEC-1993; 93WO-US12679.
9	50.0	8 20	AY08147	XX	XX	XX	PR 30-DEC-1992; 92US-0997727.
10	50.0	8 20	AY08148	XX	XX	XX	PA (RATH/) RATH M.
11	50.0	8 20	AY08149	XX	XX	XX	PI Rath M;
					XX	XX	DR WPI; 1994-249399/30.
					XX	XX	PT Identifying peptide signal sequences in a protein - and use of their synthetic analogues for treating or preventing, e.g. cardiovascular and auto-immune disease, infections and cancer.
					XX	XX	PT cardiovacular
					XX	XX	PT hepatitis C virus
					XX	XX	PT clotting factor VI
					XX	XX	PT clotting factor VII
					XX	XX	PT Human hepreceptor
					XX	XX	PT Residues 314-320 o
					XX	XX	PT Non-polio enterovi
					XX	XX	PT Coxackievirus A V
					XX	XX	PT Insulin like growt
					XX	XX	PT Human protein frag
					XX	XX	PT Human protein frag
					XX	XX	PT Heptapeptide M4.
					XX	XX	PT Human insulin
					XX	XX	PT Human UI1/UI2 split
					XX	XX	PT peptide #3 used to
					XX	XX	PT PH60(c-src) kinase
					XX	XX	PT HIV-1 pol peptide
					XX	XX	PT SEQ ID NO 438 from
					XX	XX	PT Mouse polyoma mid
					XX	XX	PT Murine TC-CSF ince
					XX	XX	PT Peptide ligand bin
					XX	XX	PT Synthetic hexapept
					XX	XX	PT S. solfatitic tr
					XX	XX	PT Kringle 5 peptide
					XX	XX	PT Human Kringle 5 pe
					XX	XX	PT Tyrosine phosphope
					XX	XX	PT SH2-binding peptid
					XX	XX	PT Immunogenic peptid
					XX	XX	PT Peptide Wif 88-95.
					XX	XX	PT Cell epitope/MHC
					XX	XX	PT Vir-derived HIV pr
					XX	XX	PT Mouse immunoglobul

ALIGNMENTS

Clotting factor VI

Human hepreceptor

Residues 314-320 o

Non-polio enterovi

Coxackievirus A V

Insulin like growt

Human protein frag

Human protein frag

Heptapeptide M4.

Human UI1/UI2 split

peptide #3 used to

PH60(c-src) kinase

HIV-1 pol peptide

SEQ ID NO 438 from

Mouse polyoma mid

Murine TC-CSF ince

Peptide ligand bin

Human plasminogen

Orotensin-IIR cycli

Recombinant timoth

kringle 5 peptide

proteo(c-src) kinase

SH2-binding peptid

Immunogenic peptid

Peptide Wif 88-95.

T cell epitope/MHC

Vir-derived HIV pr

Mouse immunoglobul

The sequence is that of a peptide signal sequence which can be used to treat diseases involving human leucocyte interterrons, including cancer, immunodeficiencies and infectious diseases.
See also AAR5944-83.

SQ	Sequence	6 AA;
QY	Query Match	61.9%; Score 26; DB 15; Length 6;
XX	Best Local Similarity	100.0%; Pred No. 4.3e+05;
Db	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AAB36378	ID	AAE05552 standard; Peptide; 6 AA.
AC	AC	AAB36378;
XX	DT	27-FEB-2001 (first entry)
DE	DE	Rat SmLIM/CRP2 putative nuclear localisation signal SEQ ID NO:15.
XX	KW	Hypertension; inhibition; treatment; SmLIM; CRP; LIM domain; smooth muscle cell LIM; vascular smooth muscle cell; hypertensive.
XX	OS	Rattus sp.
XX	PP	05-MAY-2000; 200000-0512189.
PR	PR	05-MAY-1999; 990US-0305839.
XX	PD	09-NOV-2000.
PA	PA	(HARD) HARVARD COLLEGE.
XX	PT	Lee M, Yet S;
XX	PT	Novel nucleic acid encoding a regulatory sequence which acts preferentially in vascular smooth muscle cells, operatively linked to an antisense template, used to treat hypertension
PT	PS	Disclosure; Page 33; 91pp; English.
XX	CC	The present invention describes a nucleic acid, comprising a sequence at least 50 % identical to a mouse SmLIM/CRP2 promoter cis-acting regulatory sequence, operably linked to an antisense template complementary to part of an mRNA encoding a vascular smooth muscle cell polypeptide. The first sequence directs expression of the second polypeptide. The first sequence directs expression of the second polypeptide in vascular smooth muscle cells. Also described are:
CC	CC	(1) screening candidate compounds to identify a compound capable of decreasing expression of SmLIM/CRP2 in vascular smooth muscle cells, comprising: (a) contacting a vascular smooth muscle cell with a candidate compound; and (b) determining the amount of SmLIM/CRP2 expression in the cell; and (2) a transgenic non-human mammal, the germ cells and somatic cells of which comprise a null mutation in a gene encoding SmLIM. The nucleic acids can be used for identifying compounds that decrease expression of SmLIM/CRP2 in vascular smooth muscle cells. Compounds that reduce the expression of SmLIM can be used to decrease hypertension in mammals. Compounds that reduced SmLIM activity can be used to inhibit hypertension in mammals AAC64704 to AAC64723 and AAB36370 to AAB36384 represent sequences used in the exemplification or the present invention.
XX	CC	The sequence is that of a peptide signal sequence which can be used to treat diseases involving human leucocyte interterrons, including cancer, immunodeficiencies and infectious diseases. See also AAR5944-83.
SQ	Sequence	6 AA;

QY	Query Match	57.1%; Score 24; DB 21; Length 6;
XX	Best Local Similarity	80.0%; Pred No. 4.3e+05;
Db	Matches	4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
AAB36378	ID	AAE05552 standard; peptide; 6 AA.
AC	AC	AAB36378;
XX	DT	24-SEP-2001 (first entry)
DE	DE	NLS of rat smooth muscle cell LIM (smLIM/CRP2) protein.
XX	KW	Rat; smooth muscle cell LIM; smLIM/CRP2 protein; arteriosclerosis; neointima formation; balloon angioplasty; vascular disease; cardiac; angiogenesis; peripheral vascular disease; coronary artery disease; gene therapy; antisense therapy; nuclear localisation signal; NLS.
XX	OS	Rattus sp.
PN	PN	US6258557-B1.
XX	PD	10-JUL-2001.
XX	PF	14-MAR-1997; 97US-0818655.
XX	PR	15-MAR-1996; 96US-0616368.
XX	PA	(HARD) HARVARD COLLEGE.
XX	PT	Lee M, Haber E, Jain M, Yet S;
XX	DR	WPI; 2001-450366/4B.
XX	PT	Isolated DNA encoding smooth muscle cell LIM (SmLIM/CRP2) useful for inhibiting arterial smooth muscle proliferation and for treating peripheral vascular disease, arteriosclerosis and coronary artery disease -
XX	PT	isolated DNA encoding smooth muscle cell LIM (SmLIM/CRP2) useful for inhibiting arterial smooth muscle proliferation and for treating peripheral vascular disease, arteriosclerosis and coronary artery disease -
PS	PS	Disclosure; Column 19; 38pp; English.
XX	CC	The invention relates to an isolated DNA which regulates vascular smooth muscle cell-specific transcription of a polypeptide-encoding sequence to which it is operably linked. The invention is based on the identification and characterisation of a smooth muscle cell LIM (SmLIM/CRP2) polypeptide which is expressed preferentially in arterial smooth muscle cells. SmLIM/CRP2 sequence is useful for directing vascular smooth muscle cell-specific expression of a polypeptide, by introducing vector comprising SmLIM/CRP2 into a vascular smooth muscle cell and maintaining cell under conditions suitable for polypeptide expression. SmLIM/CRP2 is useful for inhibiting arterial smooth muscle proliferation and for inhibiting neointima formation after balloon angioplasty. SmLIM/CRP2 nucleotide sequence is useful for increasing the level of SmLIM/CRP2 polypeptide in injured vascular tissues for inhibiting proliferation of smooth muscle cells. SmLIM/CRP2 is useful in gene therapy and antisense therapy for treating vascular diseases such as arteriosclerosis, and to promote angiogenesis to treat diseases such as peripheral vascular disease or coronary artery disease. The present sequence is nuclear localisation signal (NLS) of rat smooth muscle cell LIM (smLIM/CRP2) protein.
SQ	Sequence	6 AA;

Query Match 57.1%; Score 24; DB 22; Length 6;

OM protein - protein search, using sw model
Run on: January 17, 2002, 12:14:15 ; Search time 12.51 Seconds
(without alignments)
14.391 Million cell updates/sec

Title: US-09-424-080a-1
Perfect score: 42
Sequence: 1 LREKKYSP 8
Scoring table: * BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22501292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued.Patents.AA:*

1: /cgn2_6/podata/2/1aa/5A.COMB.pep:*

2: /cgn2_6/podata/2/1aa/5A_COMB.pep:*

3: /cgn2_6/podata/2/1aa/5A_COMB.pep:*

4: /cgn2_6/podata/2/1aa/6B.COMB.pep:*

5: /cgn2_6/podata/2/1aa/PCTUS.COMB.pep:*

6: /cgn2_6/podata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	42	100.0	8	Sequence 30, Appl
2	61.9	6	5	PCT-US93-12679-16
3	57.1	6	1	US-09-616-368A-15
4	57.1	6	4	US-09-054-998-15
5	57.1	6	4	US-08-818-655-15
6	57.1	7	4	US-08-891-271-13
7	52.4	7	3	US-08-756-849-13
8	50.0	8	4	US-08-444-18-659
9	47.6	7	3	US-08-390-453A-9
10	47.6	7	4	US-09-371-410-48
11	47.6	7	4	US-09-447-33-31
12	47.6	7	4	US-08-862-124-23
13	47.6	7	4	US-08-862-124-26
14	47.6	7	4	US-09-648-336-48
15	47.6	8	1	US-08-178-570-47
16	47.6	8	3	PCT-US95-0147-47
17	47.6	8	5	PCT-US95-0147-47
18	45.2	6	2	US-08-678-318-8
19	45.2	7	1	US-07-638-492-15
20	45.2	7	3	US-08-604-965E-10
21	45.2	7	3	US-08-604-965E-15
22	45.2	7	6	US-08-369-643-47
23	45.2	8	1	US-08-178-577-48
24	45.2	8	3	US-08-369-643-48
25	45.2	8	5	PCT-US93-00147-48
26	45.2	8	6	525287-44
27	42.9	18	22501292	residues

RESULT 1
US-08-659-204B-30
Sequence 30, Application US/08669284B
; Patent No. 5939534
; GENERAL INFORMATION:
; APPLICANT: Inoue, Makoto
; APPLICANT: Ikuuchi, Kaoru
; APPLICANT: Ishii, Yoko
; APPLICANT: Ito, Akira
; APPLICANT: Kimura, Toru
; APPLICANT: Nakayama, Chikao
; APPLICANT: No. 5939534uchi, Hiroshi
; TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGIRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669, 284B
; FILING DATE: 28-JUN-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/02269
; FILING DATE: 27-JUN-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 06-268281
; FILING DATE: 05-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 06-201504
; FILING DATE: 02-AUG-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 05-350934
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H
; REGISTRATION NUMBER: 33, 981
; REFERENCE/DOCKET NUMBER: 0-42041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)295-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-669-284B-30

Query Match , 100.0%; Score 42; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTEKKYSP 8
 Db 1 LTEKKYSP 8

RESULT 2

PCT-US93-12679-16

Sequence 16, Application PC/TUS9312679

GENERAL INFORMATION:

APPLICANT: Rath, Matthias

TITLE OF INVENTION: SYNTHETIC OLIGOBEPIDES ANALOGOUS TO PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND

TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: SHELDON & MAX

STREET: 401 Florence Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

PCT-US93-12679

CLASSIFICATION: CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT-US93-12679

FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Cranfill, Raymond B

REGISTRATION NUMBER: 32,845

REFERENCE/DOCKET NUMBER: RATH-10016PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5333

TELEFAX: 415-322-5499

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

PCT-US93-12679-16

Query Match , 61.9%; Score 26; DB 5; Length 6; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKYS 7
 Db 2 EKYS 6

RESULT 3

US-08-616-368A-15

Sequence 15, Application US/08616368A

Patent No. 5,767,626

GENERAL INFORMATION:

APPLICANT: Lee, Mu-En

APPLICANT: Haber, Edgar
 APPLICANT: Jain, Mukesh
 APPLICANT: Yet, Shaw-Fang
 TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patientin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/616,368A

FILING DATE: 15-MAR-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 05433/022001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8905

TELEX: 200154

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLogy: linear

MOLECULE TYPE: protein

US-08-616-368A-15

Query Match , 57.1%; Score 24; DB 1; Length 6;

Best Local Similarity 80.0%; Pred. No. 1.6e+05; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKYS 8
 Db 1 KKYG 5

RESULT 4

US-09-054-298-15

Sequence 15, Application US/09054298

Patent No. 6,136,953

GENERAL INFORMATION:

APPLICANT: Lee, Mu-En

APPLICANT: Haber, Edgar

APPLICANT: Jain, Mukesh

APPLICANT: Yet, Shaw-Fang

TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,298

US-08-818-655-15

FILING DATE: 02-APR-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/616,368
 FILING DATE: 15-MAR-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Beattie, Ph.D., Ingrid A.
 REGISTRATION NUMBER: P-42,306
 REFERENCE/DOCKET NUMBER: 05433/022002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEX: 617/542-8906

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 KKYSP 8
 |||||
 Db 1 KKYGP 5

US-08-891-271-13

Query Match 57.1%; Score 24; DB 4; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 KKYSP 8
 |||||
 Db 1 KKYGP 5

RESULT 6
 US-08-891-271-13
 Sequence 13, Application US/08891271
 Patent No. 6165476
 GENERAL INFORMATION:
 APPLICANT: Strom, Terry B.
 ATTORNEY: Sytkowski, Arthur J.
 APPLICANT: Zheng, Xin Xiao
 TITLE OF INVENTION: Fusion Proteins with an Immunoglobulin
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Milnitia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 10-JUL-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Hogle, Doreen M.
 REGISTRATION NUMBER: 36,361
 REFERENCE/DOCKET NUMBER: BIH97-07
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-891-271-13

US-08-756-849-123

Query Match 57.1%; Score 24; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.6e+05; 0; Mismatches 2; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 EKKYSP 8
 |||||
 Db 1 ESKYGP 6

RESULT 7
 US-08-756-849-123
 Sequence 123, Application US/08756849
 Patent No. 6093810
 GENERAL INFORMATION:
 APPLICANT: Bird, David Mck.
 ATTORNEY: Wilson, Mark A.
 TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 5
 US-08-818-655-15
 Sequence 15, Application US/08818655
 Patent No. 6258557
 GENERAL INFORMATION:
 APPLICANT: Lee, Mu-En
 APPLICANT: Haber, Edgar
 APPLICANT: Jain, Mukesh
 APPLICANT: Yet, Shaw-Fang
 TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Windows⁹⁵
 SOFTWARE: Fast-SEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,655
 FILING DATE: 14-MAR-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/616,368
 FILING DATE: 15-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 05433/030001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEX: 617-542-8906
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-891-271-13

CORRESPONDENCE ADDRESS: 129

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE: 08-FEB-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,474
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774

TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 023070-053510US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

FORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: linear

TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-444-818-659

Query Match 50.0%; Score 21; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gap 0;

Qy	1 TTEKKY 6	1 LITERLY 6
Db	:	:

RESULT 9
US-08-390-353A-9
; Sequence 9, Application US/08390353A
; Patent No. 6107457

GENERAL INFORMATION:
APPLICANT: Arlinghaus, Ralph B.
APPLICANT: Liu, Jiaxin
APPLICANT: Lu, Da
APPLICANT: Lopez-Berestein, Gabriel

TITLE OF INVENTION: Bor-AbL Directed Compositions and Uses for Regulating Philadelphia Chromosome Stimulated Cell Activity

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,353A
FILING DATE: 16-FEB-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732

REFERENCE/DOCKET NUMBER: UTSC:421/MAY

TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A

FORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-353A-9

Query Match 47.6%; Score 20; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1;

Qy 4 KKYSP 8
Db 1 RSYSP 5

RESULT 10
US-09-371-710-48
; Sequence 48, Application US/09371710A
; Patent No. 6146868
; GENERAL INFORMATION:
; APPLICANT: Korel, Thomas R.
; APPLICANT: Bloomer, Sharrri L.
; APPLICANT: Savoy, Anne C.
; TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of
FILE REFERENCE: DE245
CURRENT APPLICATION NUMBER: US/09/371,710A
CURRENT FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 50

SEQ ID NO 48
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: associated amino acid sequence of PCR primer 34-mer
US-09-371-710-48

Query Match 47.6%; Score 20; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KYSP 8
Db 2 KYAP 5

RESULT 11
US 09 147-933-31
; Sequence 31, Application US/09147933A
; Patent No. 6168917
; GENERAL INFORMATION:
; APPLICANT: Kilpatrick, David
TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
FILE REFERENCE: 62242-US
CURRENT APPLICATION NUMBER: US/09/147,933A
CURRENT FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: PCT/US97/17734
EARLIER FILING DATE: 1997-10-01
EARLIER APPLICATION NUMBER: U. S. 60/027,353
EARLIER FILING DATE: 1996-10-02
NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide
US-09-147-933-31

RESULT 13
US-08-862-124-26
; Sequence 26, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ZIF: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608 20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPLOGY: linear
MOLECULE TYPE: protein
US-08-862-124-23

Query Match 47.6%; Score 20; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1;

Qy 5 KYSP 8
Db 3 RYSP 6

ADDRESSEE: Morrison & Foerster LLP
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/862,124
 FILING DATE: 22 MAY 1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Lehardt, Susan K.
 REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein

US-08-862-124-26

Query Match 47.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.6e+05; Mismatches 3; Conservative 1; Indels 0;

Qy 5 KYSP 8
 Db 3 RYSP 6

RESULT 14

US-09-648-386-48

Sequence 48, Application US/09648386

Patent No. 6284508

GENERAL INFORMATION:
 APPLICANT: Bloomer, Sherri L.
 APPLICANT: Savoy, Anne C.

TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of Cryptococcus neoformans and Uses Thereof

FILE REFERENCE: D6245D

CURRENT APPLICATION NUMBER: US/09/648 386

CURRENT FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 09/371,710

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 48

LENGTH: 7

TYPE: PRT

FEATURE: ORGANISM: Artificial sequence

OTHER INFORMATION: associated amino acid sequence of PCR primer 34-mer

us-09-648-386-48

Query Match 47.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.6e+05; Mismatches 3; Conservative 1; Indels 0; Gaps 0;

Qy 5 KYSP 8
 Db 2 KYAP 5

RESULT 15

US-08-178-570-47

Sequence 47, Application US/08178570

Patent No. 5532167

GENERAL INFORMATION:
 APPLICANT: Lewis C. Cantley
 APPLICANT: Zhou Song Yang

TITLE OF INVENTION: Substrate Specificity of Protein Kinases

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 STATE STREET, suite 510
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/178-570
 FILING DATE: JANUARY 7, 1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: DeConti, Giulio A., Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-004

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-178-570-47

Query Match 47.6%; Score 20; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+05; Mismatches 3; Conservative 2; Indels 1; Gaps 0;

Qy 3 EKYSP 8
 Db 1 EEEYMP 6

Search completed: January 17, 2002, 12:16:07
 Job time: 112 sec